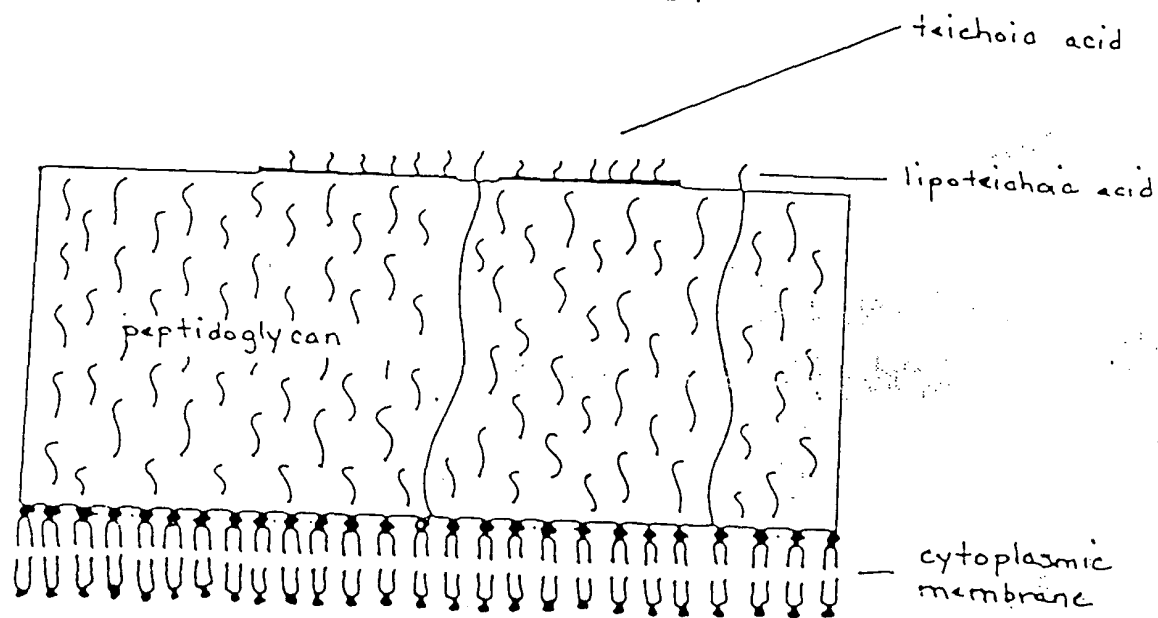
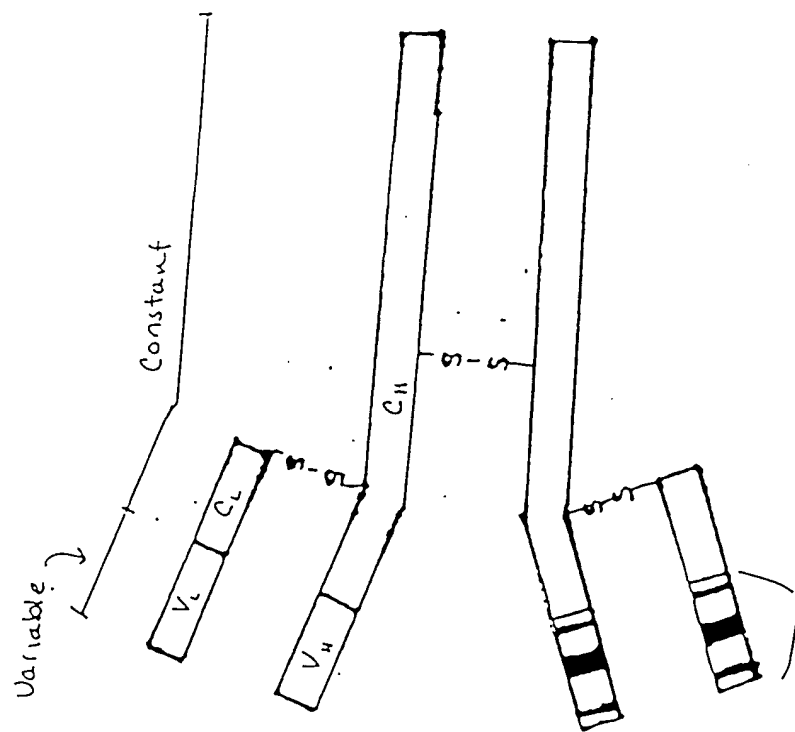


FIGURE 1



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FIGURE 2



Hypervariable regions  
Containing 3 CDRs

FIGURE 3

Effect of Anti-Staph MAB 96-110 on  
Survival in a Lethal *S. aureus* Sepsis Model

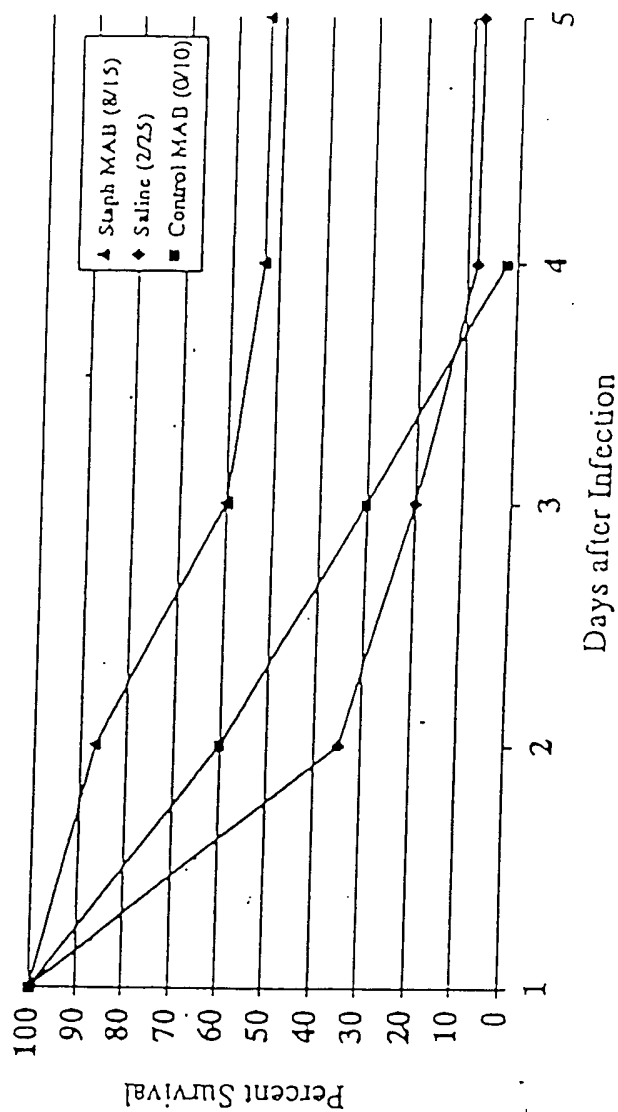


FIGURE 4

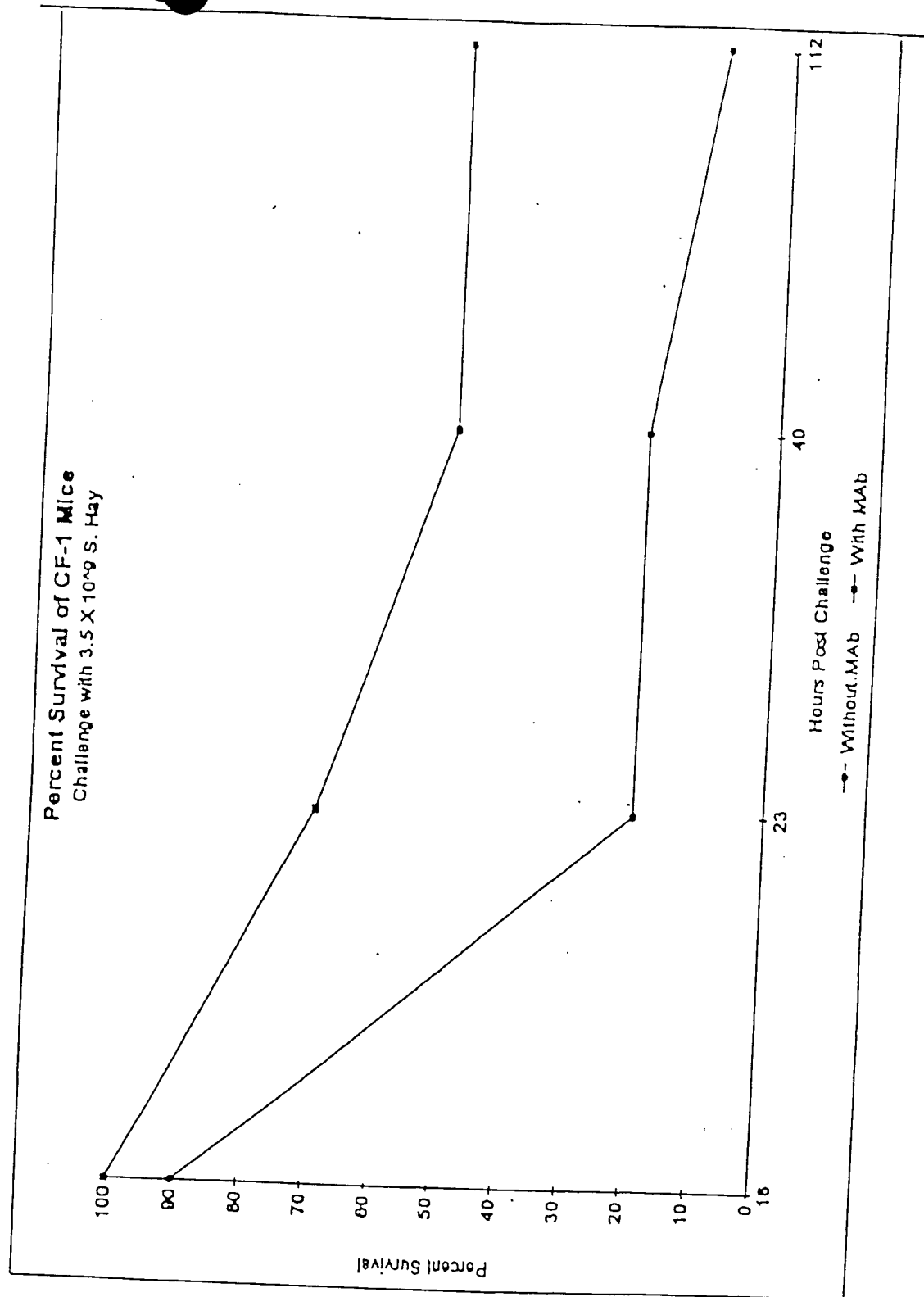


FIGURE 5

6MER_SEQ		10	20	30	
61	13.6mer2-1	GGGGCTCATC	CGGATAGGGT	TTATGGGGCC	SEQ ID NO. 4
		C A H A D R V Y G A			SEQ ID NO. 5
62	14.6mer2-2	GGGGCTCATC	CGGATAGGGT	TTATGGGGCC	
		C A H A D R V Y G A			
65	15.6mer2-3	GGGGCTCATC	CGGATAGGGT	TTATGGGGCC	
		C A H A D R V Y G A			
66	16.6mer2-4	GGGA-TCAIG	CGGATAGGGT	TTATGGGGCC	SEQ ID NO. 6
67	17.6mer2-5	GGGGCTCATC	CGGATAGGGT	TTATGGGGCC	SEQ ID NO. 7
		C A H A D R V Y G A			
68	18.6mer2-6	GGGGCTCATC	CGGATAGGGT	TTATGGGGCC	
		C A H A D R V Y G A			
69	19.6mer2-7	GGGGCTCATC	CGGATAGGGT	TTATGGGGCC	
		C A H A D R V Y G A			
70	20.6mer2-8	GGGGCTCATC	CGGATAGGGT	TTATGGGGCC	
		C A H A D R V Y G A			
71	21.6mer2-9	GGGGCTCATC	CGGATAGGGT	TTATGGGGCC	
		C A H A D R V Y G A			
72	22.6mer2-1	GGGGCTCATC	CGGATAGGGT	TTATGGGGCC	
		C A H A D R V Y G A			
73	23.6mer2-2	GGGGCTCATC	CGGATAGGGT	TTATGGGGCC	
		C A H A D R V Y G A			
74	24.6mer2-3	GGGGCTCATC	CGGATAGGGT	TTATGGGGCC	
		C A H A D R V Y G A			
75	25.6mer2-4	GGGGCTCATC	CGGATAGGGT	TTATGGGGCC	
		C A H A D R V Y G A			
76	26.6mer2-5	GGGGCTCATC	CGGATAGGGT	TTATGGGGCC	
		C A H A D R V Y G A			
77	27.6mer2-6	GGGGCTCATC	CGGATAGGGT	TTATGGGGCC	
		C A H A D R V Y G A			
78	28.6mer2-7	GGGGCTCATC	CGGATAGGGT	TTATGGGGCC	
		C A H A D R V Y G A			
79	29.6mer2-8	GGGGCTCATC	CGGATAGGGT	TTATGGGGCC	
		C A H A D R V Y G A			
80	30.6mer2-9	GGGGCTCATC	CGGATAGGGT	TTATGGGGCC	
		C A H A D R V Y G A			
81	31.6mer2-1	GGGGCTCATC	CGGATAGGGT	TTATGGGGCC	
		C A H A D R V Y G A			
82	32.6mer2-2	GGGGCTCATC	CGGATAGGGT	TTATGGGGCC	
		C A H A D R V Y G A			

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FIGURE 6

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15MER2.SEQ		10	20	30	40	50	60
50	07.15mer2-1/0	GGGGCTTGGC	ATTGGCGTCA	TCGTATTCCT	CTTCAGCTTG	CTGCTGGTCG	TGGGGCC SEQ ID NO. 8
70		G A W H W R H R I P L Q L A A G R	G A				SEQ ID NO. 9
52	09.15mer2-3/0	GGGGCTCGTC	GGCATCGTAA	TTTTTTCAT	TTTTTTCATC	GGTCGTTGAT	TGGGGCC SEQ ID NO. 10
72		G A R R H G N F S H F F H R S L I	C A				SEQ ID NO. 11
53	10.15mer2-4/0	GGGGCTTGA	GGGTTTCTT	TATTCATCT	TATCGTCC	CGGGTTCGGC	TGGGGCC SEQ ID NO. 12
73		G A W K A L F S H S Y R P R G S A	G A				SEQ ID NO. 13
54	11.15mer2-5/0	GGGGCTAGGC	ATTGGCGTCA	TCGTATTCCT	CTTCAGCTTG	CTGCTGGTCG	TGGGGCC SEQ ID NO. 14
74		G A R H W R H R I P L O L A A G R	C A				SEQ ID NO. 15
56	13.15mer2-7/0	GGGGCTTGGC	ATTGGCGTCA	TCGTATTCCT	CTTCAGCTTG	CTGCTGGTCG	TGGGGCC SEQ ID NO. 16
76		G A W H W R H R I P L O L A A G R	C A				SEQ ID NO. 17
57	14.15mer2-8/0	GGGGCTTGGC	ATTGGCGTCA	TCGTATTCCT	CTTCAGCTTG	CTGCTGGTCG	TGGGGCC SEQ ID NO. 18
77		G A W H W R H R I P L O L A A G R	C A				SEQ ID NO. 19
58	15.15mer2-9/0	GGGGCTCACC	TGGCTGTTT	CTATCCTCT	TTGCTCATC	CTACTGACCT	TGGGGCC SEQ ID NO. 20
78		G A Q V A V L Y P P L A D A T E L	C A				SEQ ID NO. 21
59	16.15mer2-10/0	GGGGCTCGTC	GGCATCGTAA	TTTTTTCAT	TTTTTTCATC	GGTCGTTGAT	TGGGGCC SEQ ID NO. 22
79		G A R R H G N F S H F F H R S L I	G A				SEQ ID NO. 23
60	17.15mer2-11/0	GGGGCTCGTC	GGCATCGTAA	TTTTTTCAT	TTTTTTCATC	GGTCGTTGAT	TGGGGCC SEQ ID NO. 24
80		G A R R H G N F S H F F H R S L I	G A				SEQ ID NO. 25
61	18.15mer2-12/0	GGGGCTTGGC	GTATGTATT	TTTTCATCGT	CATCGGCATC	TTCTAGTCC	TGGGGCC SEQ ID NO. 26
81		G A W R M Y F S H R H A H L R S P	G A				SEQ ID NO. 27
62	19.15mer2-13/0	GGGGCTTCCC	GTATGTATT	TTTTCATCGT	CATCGGCATC	TTCTAGTCC	TGGGGCC SEQ ID NO. 28
82		G A W R M Y F S H R H A H L R S P	G A				SEQ ID NO. 29
63	20.15mer2-14/0	GGGGCTTCCC	GGAGTATT	TTCTATCAT	CATCGGCATC	TTCTAGTCC	TGGGGCC SEQ ID NO. 30
93		G A W R K Y F S Y H H A H L C S P	G A				SEQ ID NO. 31
64	21.15mer2-15/0	GGGGCTTGGC	GTATGTATT	TTTTCATCGT	CATCGGCATC	TTCTAGTCC	TGGGGCC SEQ ID NO. 32
94		G A W R M Y F S H R H A H L R S P	G A				SEQ ID NO. 33
65	22.15mer2-16/0	GGGGCTTGGC	GTATGTATT	TTTTCATCGT	CATCGGCATC	TTCTAGTCC	TGGGGCC SEQ ID NO. 34
95		G A W R M Y F S H R H A H L R S P	G A				SEQ ID NO. 35
66	23.15mer2-17/0	GGGGCTTGGC	GTATGTATT	TTTTCATCGT	CATCGGCATC	TTCTAGTCC	TGGGGCC SEQ ID NO. 36
96		G A W R M Y F S H R H A H L R S P	G A				SEQ ID NO. 37
67	24.15mer2-18/0	GGGGCTCGTC	GGCATCGTAA	TTTTTTCAT	TTTTTTCATC	GGTCGTTGAT	TGGGGCC SEQ ID NO. 38
97		G A R R H G N F S H F F H R S L I	G A				SEQ ID NO. 39
68	25.15mer2-19/0	GGGGCTTGGC	ATTGGCGTCA	TCGTATTCCT	CTTCAGCTTG	CTGCTGGTCG	TGGGGCC SEQ ID NO. 40
98		G A W H W R H R I P L Q L A A G R	C A				SEQ ID NO. 41
69	26.15mer2-20/0	GGGGCTCGTC	GGCATCGTAA	TTTTTTCAT	TTTTTTCATC	GGTCGTTGAT	TGGGGCC SEQ ID NO. 42
99		G A R R H G N F S H F F H R S L I	G A				SEQ ID NO. 43

FIGURE 7

.SMER: .SEQ

	10	20	30	40	50	60	
1: 20.15mer1-2/	CGGGCTGATT	CGATTACTTT	TCATCGTCGT	CATCATGATC	GTGTTCTTTC	TGGGGCC	SEQ ID NO. 44
17	G A D	W I T F	H R R	H H D	R V L S	G A	SEQ ID NO. 45
12: 29.15mer1-3/	CGGGCTGATT	CGATTACTTT	TCATCGTCGT	CATCATGATC	GTGTTCTTTC	TGGGGCC	SEQ ID NO. 46
18	G A C	W I T F	H R R	H H D	R V L S	G A	SEQ ID NO. 47
15: 32.15mer1-6/	CGGGCTGATT	CGATTACTTT	TCATCGTCGT	CATCATGATC	GTGTTCTTTC	TGGGGCC	
11	G A G	W I T F	H R R	H H D	R V L S	G A	
12: 13.15mer1-7/	CGGGCTGATT	CGATTACTTT	TCATCGTCGT	CATCATGATC	GTGTTCTTTC	TGGGGCC	
16	G A G	W I T F	H R R	H H D	R V L S	G A	
13: 14.15mer1-8/	CGGGCTGATT	CGATTACTTT	TCATCGTCGT	CATCATGATC	GTGTTCTTTC	TGGGGCC	
17	G A G	W I T F	H R R	H H D	R V L S	G A	
14: 15.15mer1-9/	CGGGCTGATT	CGATTACTTT	TCATCGTCGT	CATCATGATC	GTGTTCTTTC	TGGGGCC	
18	G A C	W I T F	H R R	H H D	R V L S	G A	
15: 16.15mer1-10/	CGGGCTGATT	CGATTACTTT	TCATCGTCGT	CATCATGATC	GTGTTCTTTC	TGGGGCC	
19	G A G	W I T F	H R R	H H D	R V L S	G A	
16: 17.15mer1-11/	CGGGCTGATT	CGATTACTTT	TCATCGTCGT	CATCATGATC	GTGTTCTTTC	TGGGGCC	
10	G A C	W I T F	H R R	H H D	R V L S	G A	
17: 18.15mer1-12/	CGGGCTGATT	CGATTACTTT	TCATCGTCGT	CATCATGATC	GTGTTCTTTC	TGGGGCC	
11	G A C	W I T F	H R R	H H D	R V L S	G A	
18: 19.15mer1-13/	CGGGCTGATT	CGATTACTTT	TCATCGTCGT	CATCATGATC	GTGTTCTTTC	TGGGGCC	
12	G A C	W I T F	H R R	H H D	R V L S	G A	
19: 20.15mer1-14/	CGGGCTGATT	CGATTACTTT	TCATCGTCGT	CATCATGATC	GTGTTCTTTC	TGGGGCC	
13	G A G	W I T F	H R R	H H D	R V L S	G A	
10: 21.15mer1-15/	CGGGCTGATT	CGATTACTTT	TCATCGTCGT	CATCATGATC	GTGTTCTTTC	TGGGGCC	
14	G A G	W I T F	H R R	H H D	R V L S	G A	
11: 22.15mer1-16/	CGGGCTGATT	CGATTACTTT	TCATCGTCGT	CATCATGATC	GTGTTCTTTC	TGGGGCC	SEQ ID NO. 48
15	G A G	K A H F	S H S	Y R H	R G S A	G A	SEQ ID NO. 49
12: 23.15mer1-17/	CGGGCTGATT	CGATTACTTT	TCATCGTCGT	CATCATGATC	GTGTTCTTTC	TGGGGCC	
16	G A C	W I T F	H R R	H H D	R V L S	G A	
13: 24.15mer1-18/	CGGGCTGATT	CGATTACTTT	TCATCGTCGT	CATCATGATC	GTGTTCTTTC	TGGGGCC	
17	G A G	W I T F	H R R	H H D	R V L S	G A	
14: 25.15mer1-19/	CGGGCTGATT	CGATTACTTT	TCATCGTCGT	CATCATGATC	GTGTTCTTTC	TGGGGCC	
18	G A G	W I T F	H R R	H H D	R V L S	G A	
15: 26.15mer1-20/	CGGGCTGATT	CGATTACTTT	TCATCGTCGT	CATCATGATC	GTGTTCTTTC	TGGGGCC	
19	G A G	W I T F	H R R	H H D	R V L S	G A	

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FIGURE 8

masterlist		10	20	30	40	50	60	70	
54	15mer 1st.1	GGGCTGATT	CGATTACTTT	TCATCTGCTT	CATCATCATC	CTCTTCTTTC	TCGCCCC	16/17	SEQ ID NO 50
57		G A D	W I T F	K R R	K H D	R V L S	G A		SEQ ID NO 51
90	15mer 1st.2	GGGCTTAGTC	GTATATATCT	TCCTCGCTCG	TCGCTTTTCC	TTCTCTCTCC	TCGCCCC	1/10	Seq ID NO 52
91		G A S	R H M L	A R W	S R L	L A V P	G A		Seq ID NO 53
71	15mer 1st.16	GGGCTTGGG	AGCTATATCT	TAGTCAATCT	TATCTCATC	GGGCTTGGC	TCGCCCC	1/17	Seq ID NO 54
85		G A G	K A M F	S H S	Y R H	R G S A	G A		Seq ID NO 55
92	15mer 2nd.1	GGGCTTGGC	ATTGGCTCA	TCGTATCTCT	CTTCAGCTTC	CTCTCTGCTC	TCGCCCC	5/18	Seq ID NO 56
98		G A W	H W R H	R I P	L Q L	A A G R	G A		Seq ID NO 57
93	15mer 2nd.3	GGGCTCTGTC	GGCATGGTAA	TTTTTCTCAT	TTTTTTCATC	GGTCTTCTAT	TCGCCCC	1/18	Seq ID NO 58
99		G A R	R H G N	F S H	F F H	R S L I	G A		Seq ID NO 59
94	15mer 2nd.4	GGGCTTGGG	AGCTTTTCTT	TAGTCAATCT	TATCTCTCTC	GGGCTTGGC	TCGCCCC	1/18	Seq ID NO 60
100		G A W	X A L F	S H S	Y R P	R G S A	G A		Seq ID NO 61
95	15mer 2nd.9	GGGCTCAGG	TCGGCTTTT	CTATCTCTCT	TTGGCTGATC	CTACTCTAGCT	TCGCCCC	1/18	Seq ID NO 62
101		G A Q	V A V L	Y P P	L A D	A T E L	G A		Seq ID NO 63
96	15mer 2nd.12	GGGCTTGGC	GTATCTATTT	TTCTCATCTG	CACTGGCATC	TTCTCTAGTCC	TCGCCCC	1/18	Seq ID NO 64
102		G A W	R M Y F	S H R	H A H	L R S P	G A		Seq ID NO 65
97	6mer 2nd.1	GGGCTCATC	CGATAGGCT	TTATCGGGC				15/18	Seq ID NO 66
103		G A H	A D R V	Y G A					Seq ID NO 67



FIGURE 9

Comparison of Signals at  $6.25 \times 10^{11}$  vir/mL.

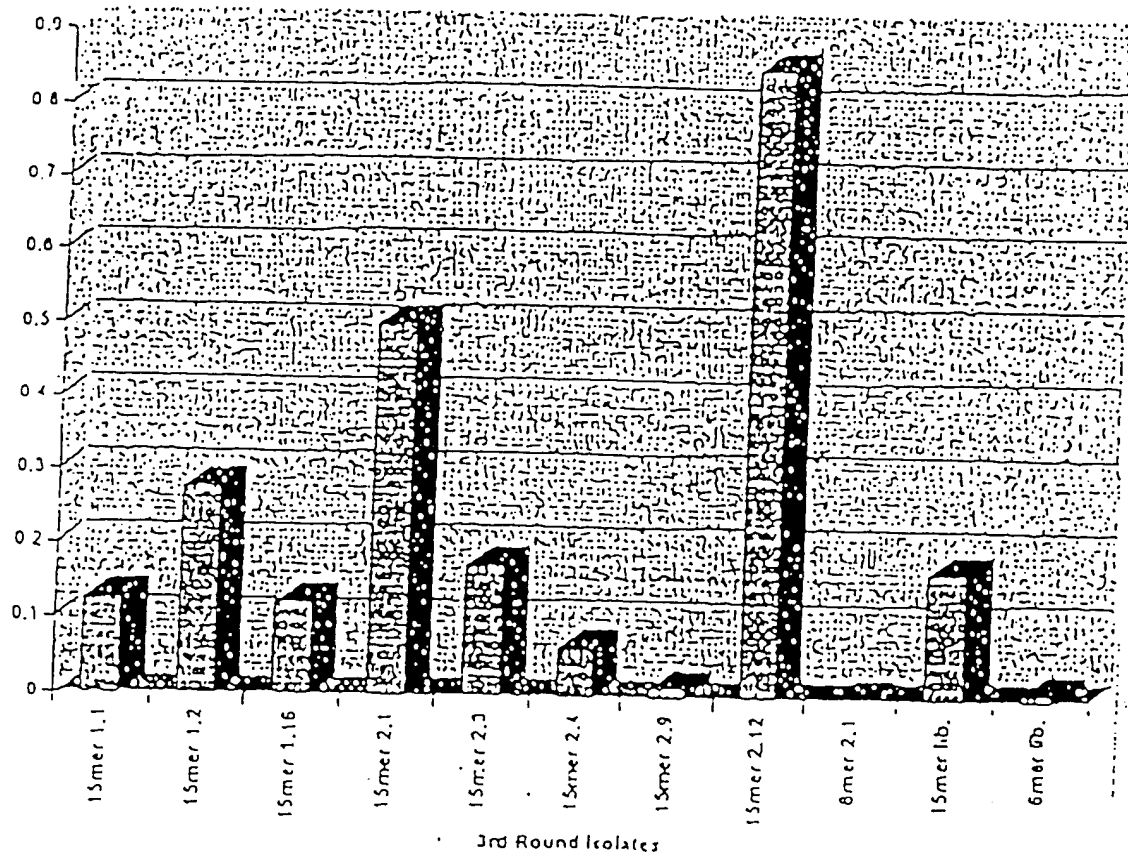
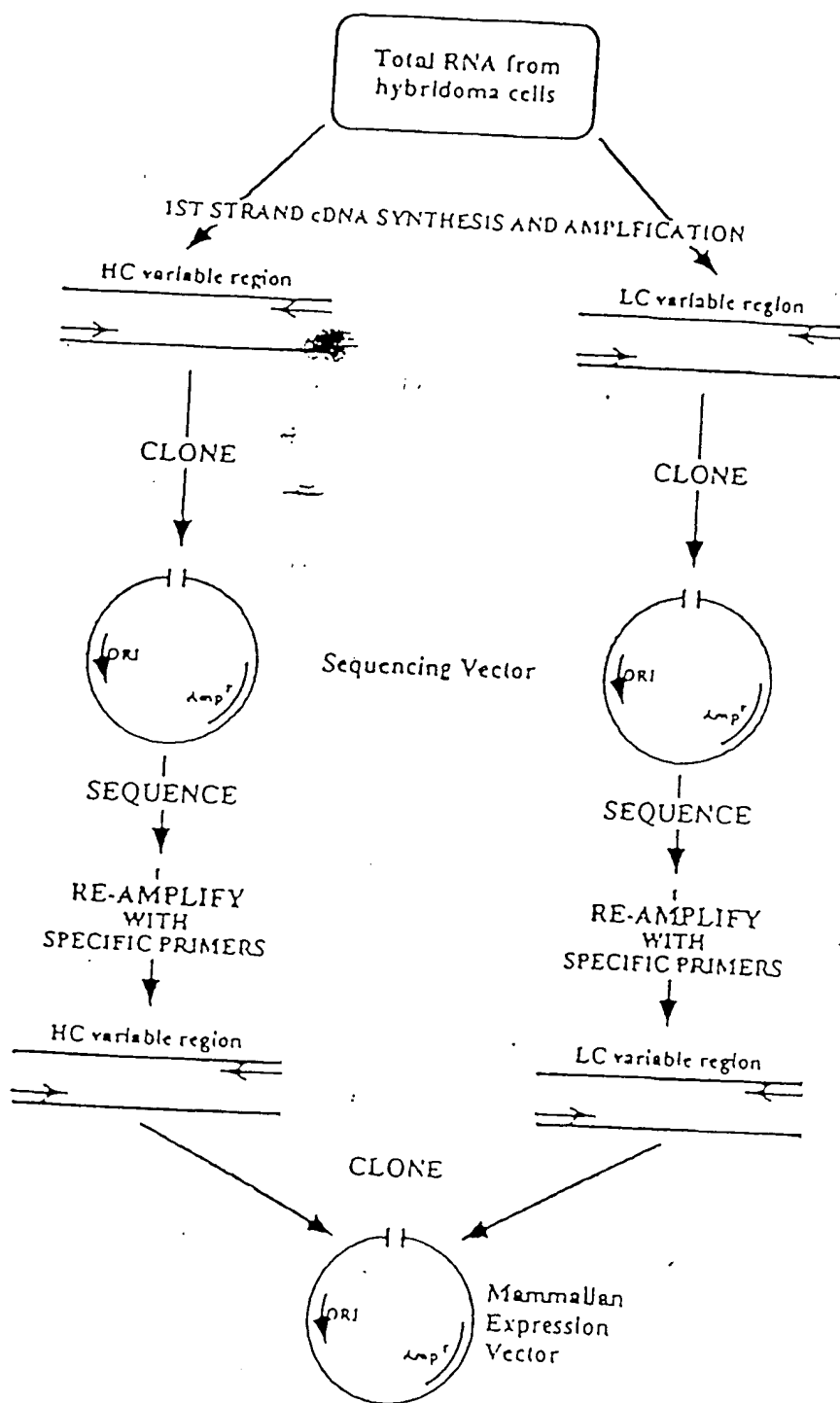


FIGURE 10: General Cloning Strategy



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FIGURE 11

*Mouse Heavy Chain "front" primers*

JSS1  
5'-ATTTCAGGCCCAGCCGGCCATGGCCGARGTRMAGCTKSAXGAGWC-3' SEQ ID NO 68  
JSS2  
5'-ATTTCAGGCCCAGCCGGCCATGGCCGARGTYCARCTKCARCARYC-3' SEQ ID NO 69  
JSS3  
5'-ATTTCAGGCCCAGCCGGCCATGGCCGAGGTGAAGCTKSTSGARTC-3' SEQ ID NO 70  
JSS4  
5'-ATTTCAGGCCCAGCCGGCCATGGCCGAVGTGMWGCTKGTGGAGWC-3' SEQ ID NO 71  
JSS8  
5'-ATTTCAGGCCCAGCCGGCCATGGCCGAGGTBCARCTKMARSARTC-3' SEQ ID NO 72

*Mouse Heavy chain "back" primers*

JS160  
5'-GCTGCCACCGCCACCTGMRGAGACDGTGASTGARG-3' SEQ ID NO 73  
JS161  
5'-GCTGCCACCGCCACCTGMRGAGACDGTQASMOTRG-3' SEQ ID NO 74  
JS162  
5'-GCTGCCACCGCCACCTGMRGAGACDGTGASCAGRG-3' SEQ ID NO 75

*Mouse Light Chain Leader "front" primers*

PMC12  
5'-CCCGGGCCACCATGGAGACAGACACACTCCTG-3' SEQ ID NO 76  
PMC13  
5'-CCCGGGCCACCATGGATTTTCAAAGTCCAAGATTTTC-3' SEQ ID NO 77  
PMC14  
5'-CCCGGGCCACCATGGAGWCACAKWCTCAGGTC-3' SEQ ID NO 78  
PMC15  
5'-CCCGGGCCACCATGKCCCCWRCTCAGYTTCTKG-3' SEQ ID NO 79  
PMC55  
5'-CCCGGGCCACCATGAAGTTGCCTGTTAGGCTG-3' SEQ ID NO 80

*Mouse Light Chain "back" primer*

OKA57  
5'-GCACCTCCAGATGTAACTGCTC-3' SEQ ID NO 81

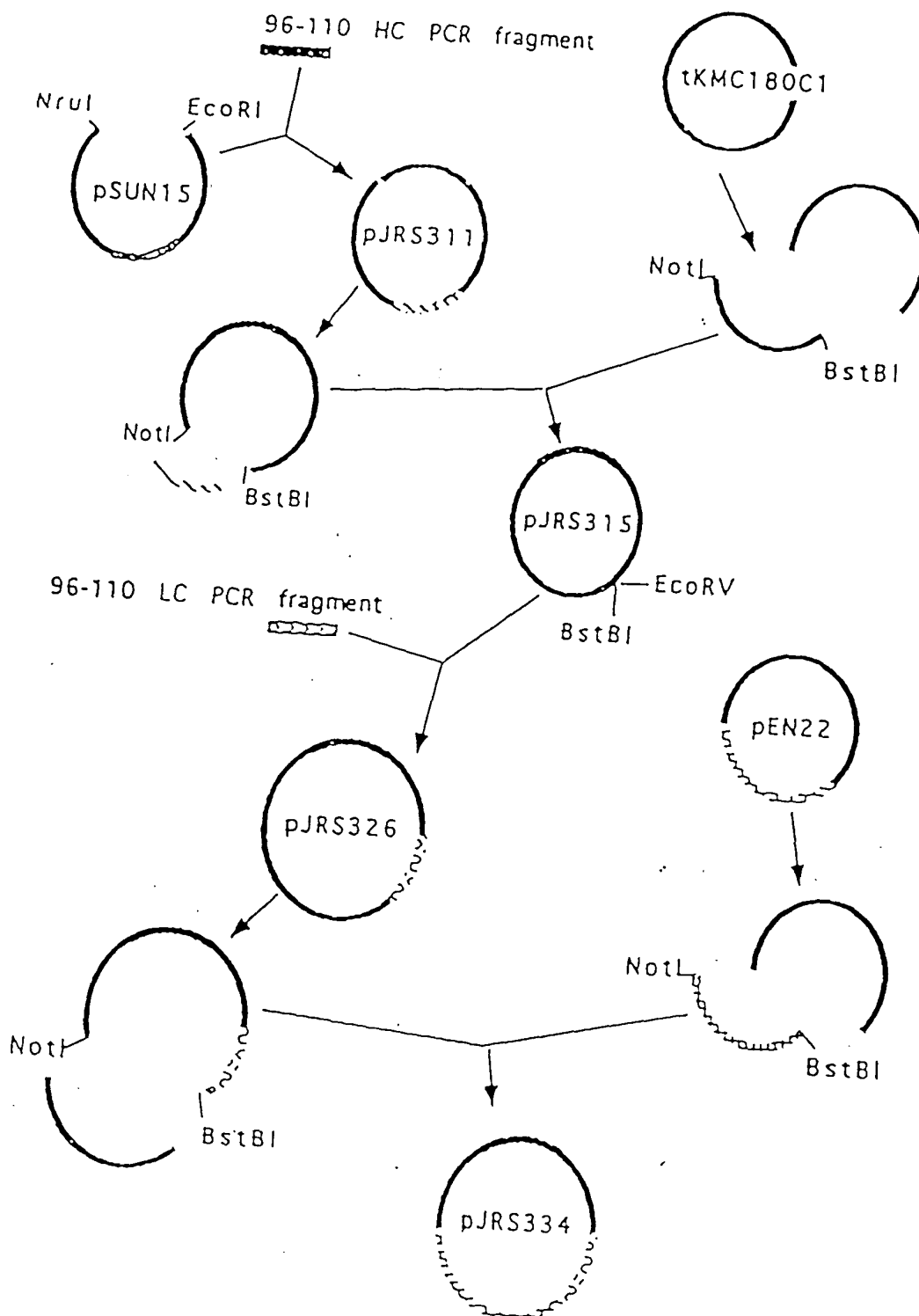
*"96-110" Specific Primers*

96110HF2  
5'-TAATATCGCGACAGCTACAGGTGTCCACTCCCGAAGTGATGCTGGTGGAGWCTG-3' SEQ ID NO 82  
96110HB  
5'-TTATAGAAATTCGTGAGGAGACGGTGAGTGAG-3' SEQ ID NO 83  
96110BLF  
5'-TTAGGCGATATTCGTTCTCTCCCACTCTCC-3' SEQ ID NO 84  
96110BLB  
5'-GTAACCGTTCCGAAAGTGTAAGTTACGTTTATTTCCAGCATGCTCC-3' SEQ ID NO 85

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FIGURE 13



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**D E F I N I T I O N**

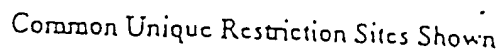


FIGURE 15: Antibody Production ELISA

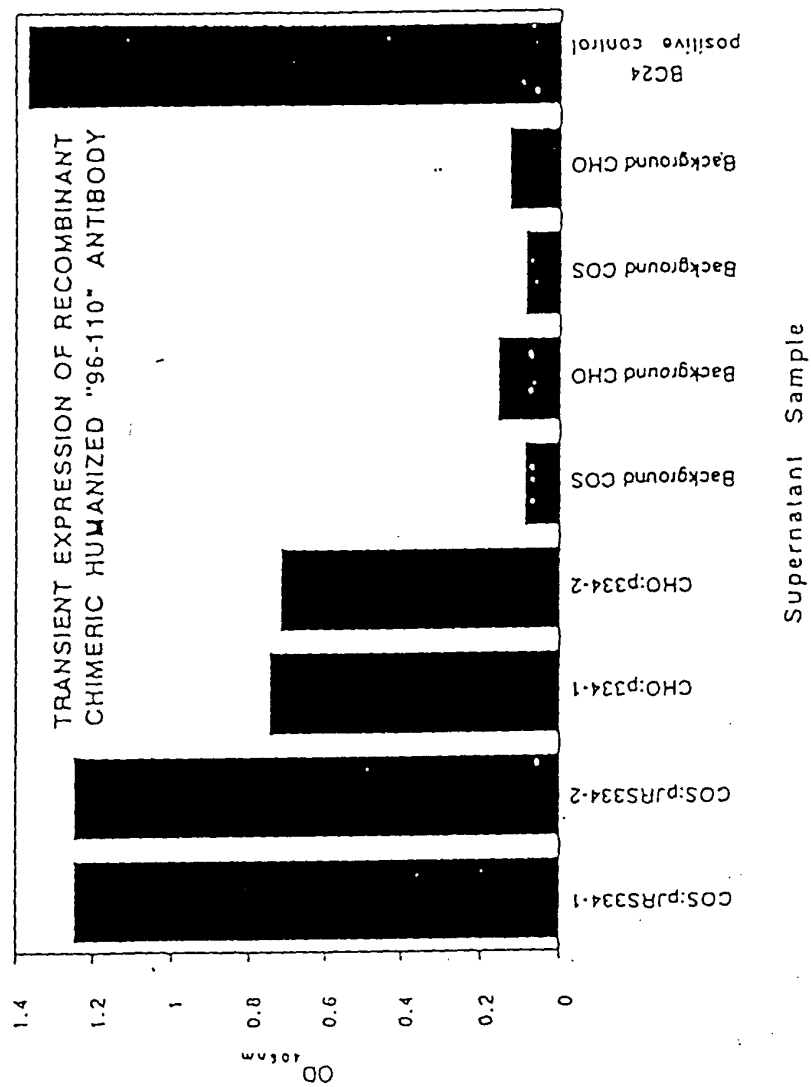
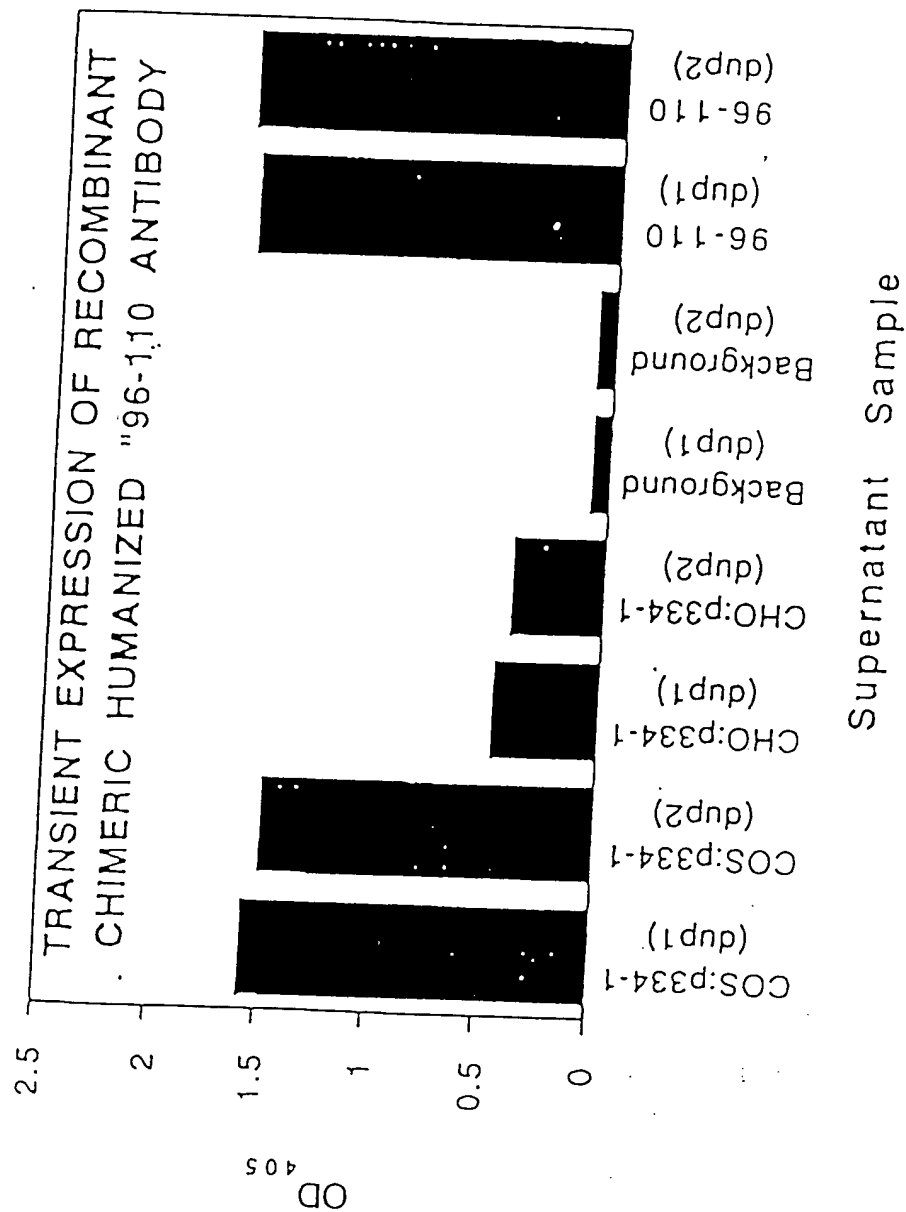
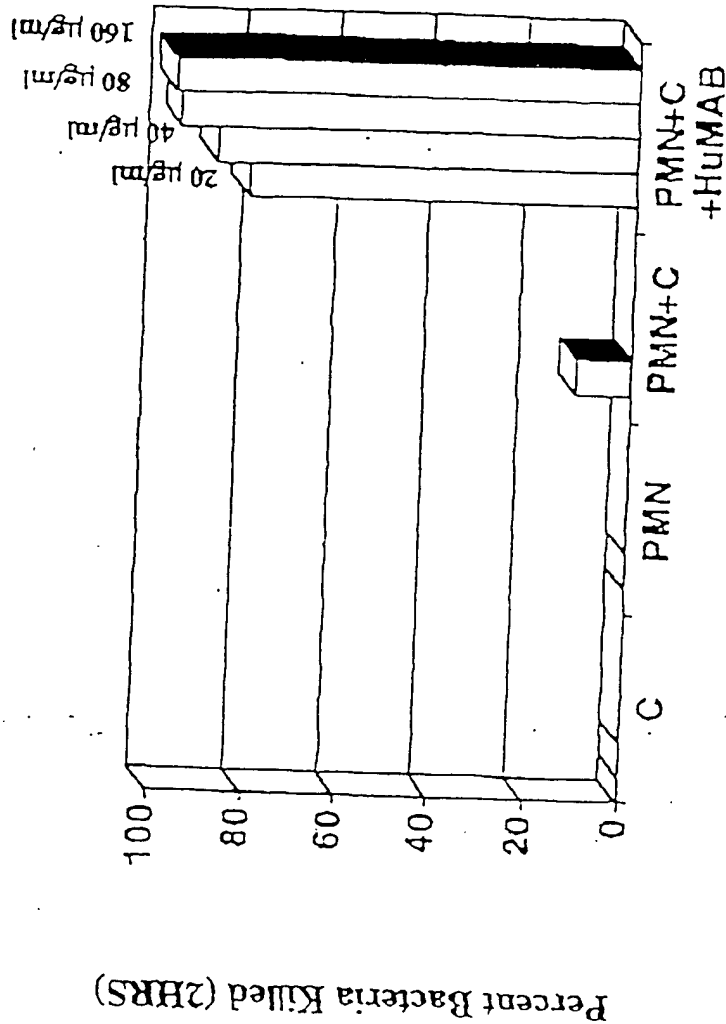


FIGURE 16: Anti-Staph HAY Activity ELISA



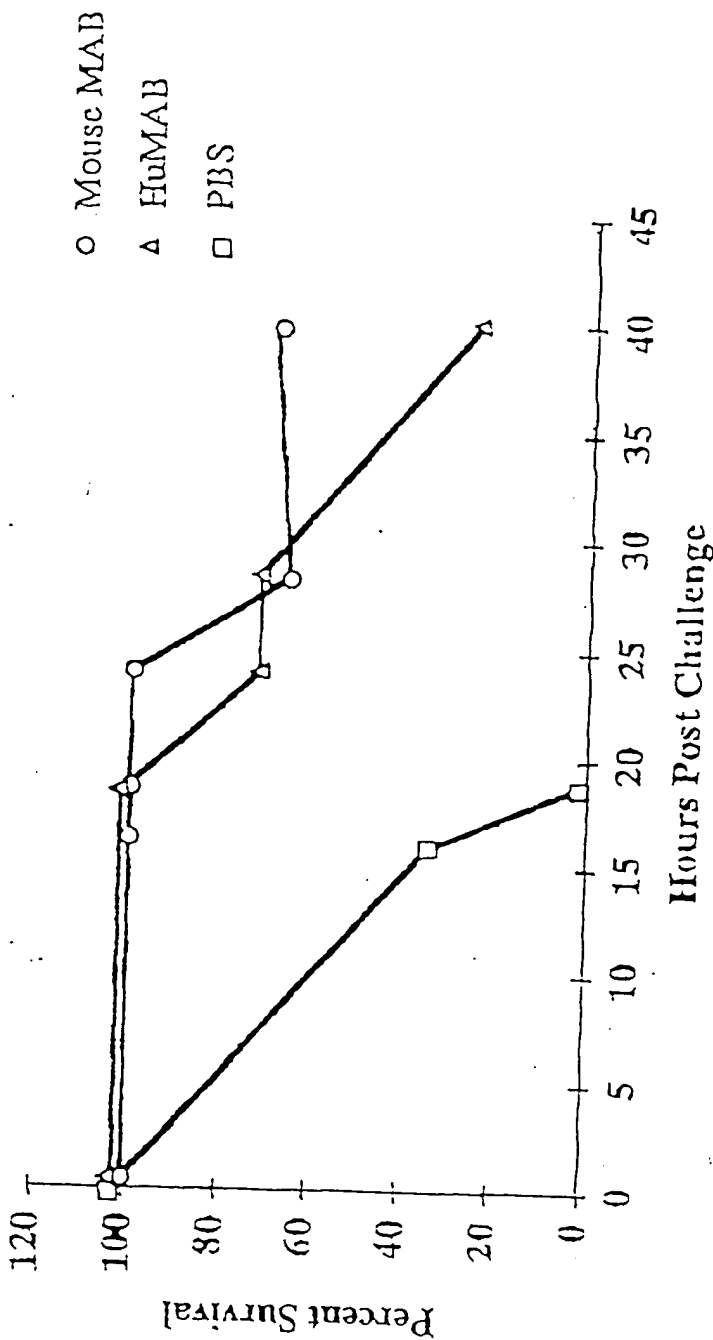


# Opsonic Activity of HuMAB 96-110 for *S.epidermidis* in a Neutrophil Mediated Opsonophagocytic Bactericidal Assay Using Human Complement



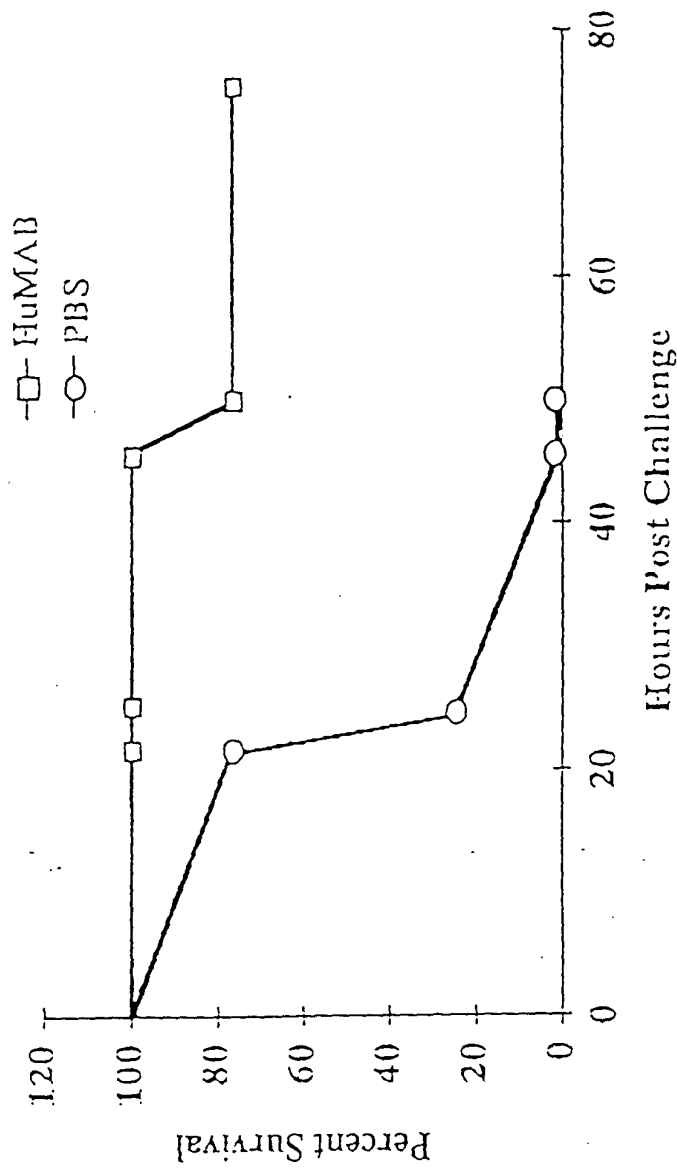
C-Barb-Ex (1:4), Human  
PMN-Human  
Bacterin-*S.epidermidis* (Strain Hay)

# Pilot Study to Compare the Effect of Mouse MAB 96-110 and HuMAB 96-110 in a Lethal Model of *S. Epidermidis* Sepsis



MAB dose: 14 mg/kg given IP, 24 and 1 Hour prior to infection

# Survival of CF-1 Mice after Intraperitoneal Challenge with $3 \times 10^9$ *S. epidermidis* (Hay)



18 mg/kg/dose, IP, 24 and 48 hours prior to infection

# Effect of HuMAB 96-110 on Bacteremia in a Lethal *S. epidermidis* Sepsis Model

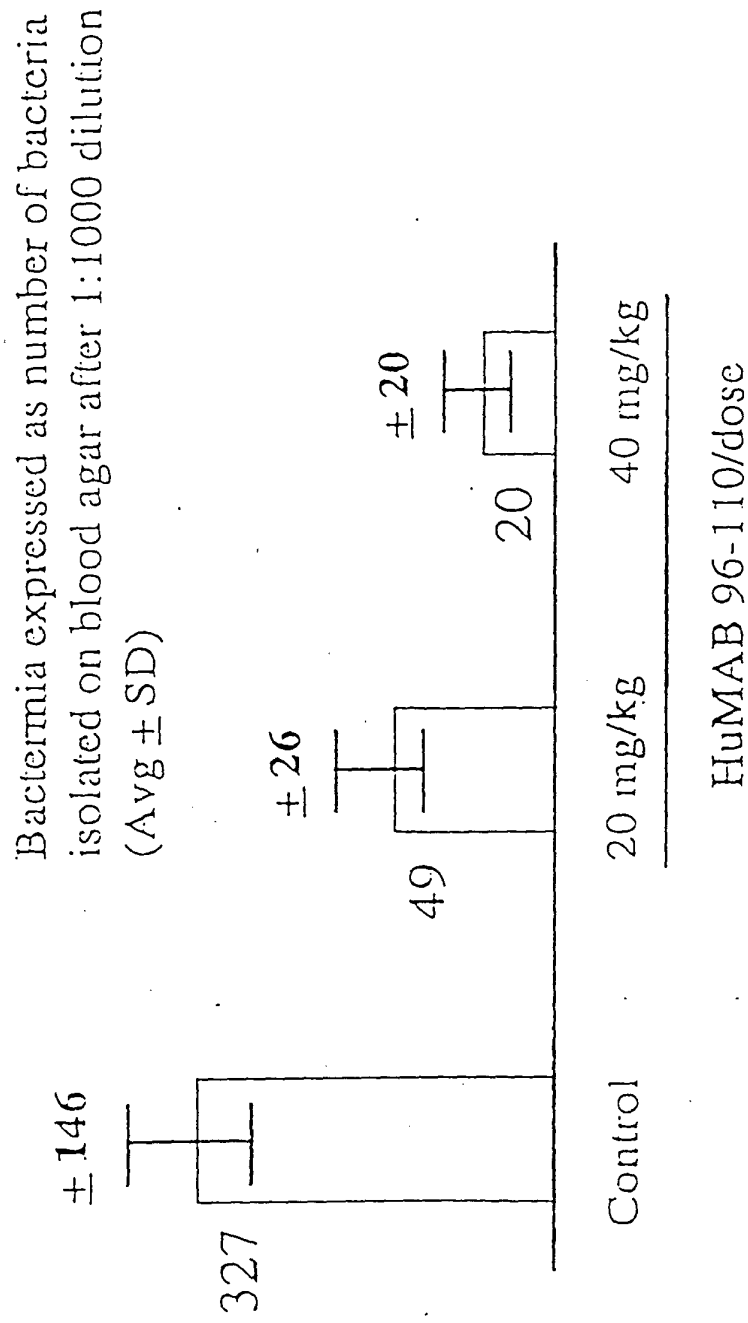
## Geometric Mean Bacteremia Level

Saline				
Placebo	$6.5 \times 10^4$	$7.2 \times 10^4$	$5.2 \times 10^4$	$7 \times 10^3$
HuMAB				
96-110	$3 \times 10^2$	$7.5 \times 10^2$	$2.1 \times 10^1$	$1.7 \times 10^1$
	4 hrs	8 hrs	12 hrs	18 hrs

## Time Post Infection

HuMAB 96-110 18 mg/kg/dose or saline given IP, 24 and 1 hour prior to IP infection with  $3 \times 10^9$  *S. epidermidis* (Hay)

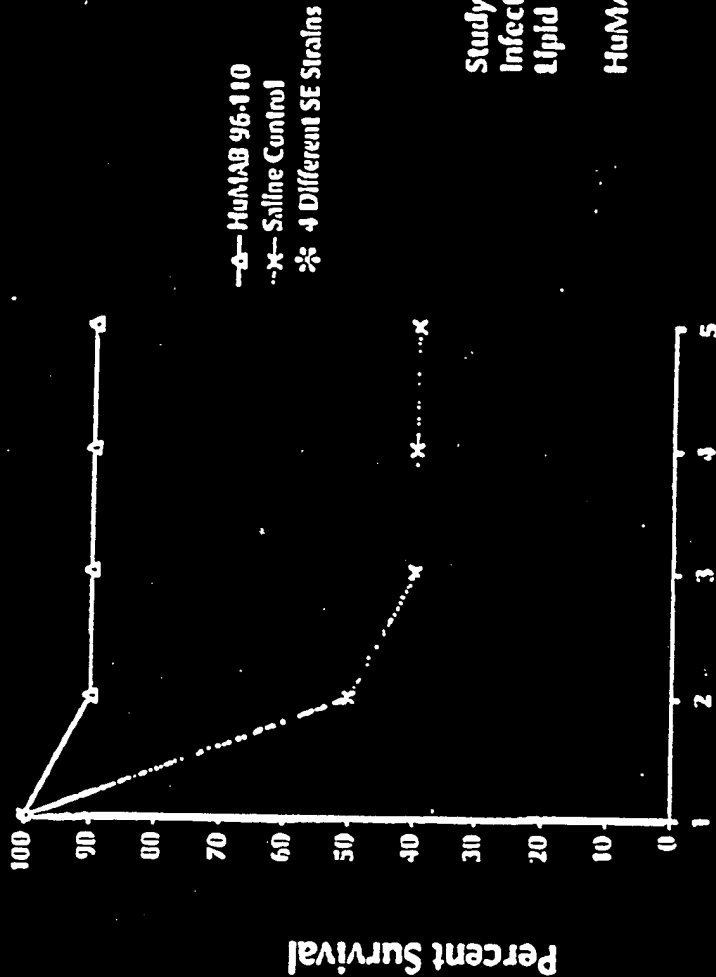
# Bacteremia levels 4 hrs after infection with $3 \times 10^9$ *S.epidermidis*\*



\* CF-1 mice infected IP with strain Hay-HuMAB given IP x 2

# The Effect of Hu 96-110 on Survival in a Lethal Neonatal *S.epidermidis*\* Sepsis Model: Study II

Survival:  
Hu 96-110 27/30 (90%)  
Saline 12/30 (40%)



## Study II:

Infection--~5x10<sup>7</sup> SE, SQ (with plastic catheter SQ)  
Lipid Emulsion - 0.2 ml, 20% IP day-1 and + 1, 2

doses day 0

HuMAB or Saline- 0.2 ml, IP 30 min before and 24 hrs after infection

Dose: 50-60 mg/kg per dose

Days After Infection

96-110 anti-staph (HAY) heavy chain variable region (type IIIA)

B V H L V H S G C G L V Q P X G G L X L S C A A S G F T P U  
 G A L G T A T G C T G C G A G C A T G C T G C A G C C T A A G G C T C A T T G A A C T C T G C A G C C T C T G C A T T C A C C T T C A A T

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CCCCTTAAAGAAAGTAAAGTAAATTAATTCGAACATTTTATATGCGGAAATCTAGTGAACAG

R P T I S R D B S Q S H L Y L O H N N L X T R D T A W Y Y C V R

XGCTTCACCAATCGATTCCAGCATGGTTCATCAGAATAAACAATGCATTTACTGTCTCAGA.

[illegible]

96-110 anti-staph (HAY) light chain variable region (type VI)

Q I V L S O S P A I L S A S P G R K V T H T C  
C A A A T T G T H C T C T C C C A G T C T C A G C A A T C T C T C T C A G G T C A C A A T C A C T T G C

3Y35i.Y3Y.f.i.YYY.i.5.i.5Y Y2I.55Y.55553Y

U X S S S V H Y H H

TGGTACGAGCGAGGCGGAGTCCTCCCCCGAACCCTCCGATTCTC  
W Y Q Q K P G S J P K P W I S A T S W L V A A

C V P A N P S C S C G T Y Y Y I J R V E X E D A A T Y Y C

CGATCCCTGCTCCCTTCAGTGGCAGCTGTCTCTCAATCATCCGACCTGAAATGCTGC

Q O W S S H P P T P C G C T W L Z I R SEQ ID NO. 89

CAGCAGTCGACGTATGTAACTCCACCCACTCCTCGAATTACGA TTCCACGCCGCACCACTCTCTCGAATTACGA SEQ ID NO. 88

CDR Regions Underlined